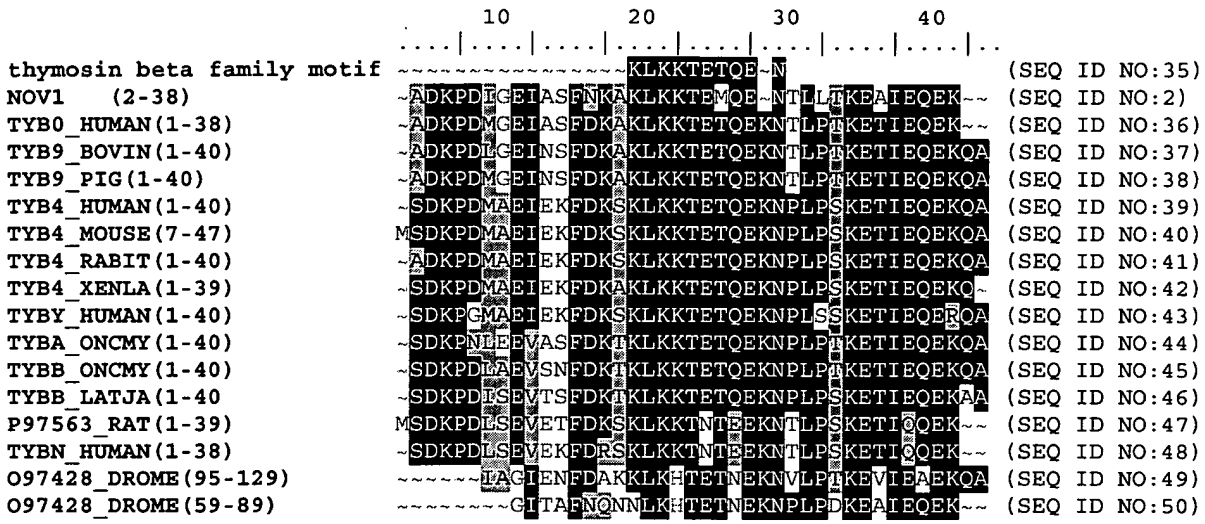
(Black outlined amino acids indicate potential regions of conserved sequence; grayed amino acids represent amino acids conservatively substituted; and non-highlighted amino acids indicate positions in which mutations to a broad range of alternative amino acid residues occurs. Sequences may be referenced by the SWISSPROT or TREMBL ID.)



On page 10, please replace Table 4 with the following Table 4:

Table 4.
PFAM alignment of a NOV1 polypeptide to the consensus sequence of the thymosin beta family

```
>PD005116 (Closest domain: TYB0_HUMAN 1-38)
Number of sequences in family: 16
Most frequent protein names:   TYB4(4) TYB9(2) TYBB(2)
Commentary (automatic):
           THYMOSIN ACETYLATION T-CELL DIFFERENTIATION
           IMMUNOPOTENTIATION THYMUS BETA-4 ACTIN-BINDING PROTEIN
           BETA
           Length = 38
  Score = 145  (60.9 bits), Expect = 5e-10
 Identities = 32/38 (84%), Positives = 34/38 (89%), Gaps = 1/38 (2%)

NOV1:      2 ADKPDIGEIASFNKAKLKKTEMQE-NTLLTKEAIEQEK 38 (SEQ ID NO:2)
             |||||+||||||+|||||||| || ||| ||| |||||
Sbjct:     1 ADKPDMGEIASFDKAKLKKTETQEKNTLPTKETIEQEK 38 (SEQ ID NO:51)
```

Beginning on page 13, kindly replace Table 6 with the following Table 6:

Table 6.
Comparison between a NOV2 polypeptide and mouse ephrin type-A receptor 8 precursor

```
>ref|NP_031965.1| Eph receptor A8
 sp|O09127|EPA8_MOUSE EPHRIN TYPE-A RECEPTOR 8 PRECURSOR (TYROSINE-PROTEIN KINASE
           RECEPTOR EEK) (EPH-AND ELK-RELATED KINASE)
 gb|AAB39218.1| (U72207) Eph-and Elk-related kinase [Mus musculus]
```

```
          Length = 1004

 Score = 3036 bits (7128), Expect = 0.0
 Identities = 945/992 (95%), Positives = 964/992 (96%), Gaps = 1/992 (0%)

NOV2:  1   MAPARGRLPPALWVVTAAAAAATCVSAARGEVNLLDTSTIHGDWGWLTYPAHGWDSINEV 60
           |||||  ||  ||||||||||||  |||||  ||||||||||||||||||||||||||||||
Sbjct:  1   MAPARARLSPALWVVTAAAAA-TCVSAGRGEVNLLDTSTIHGDWGWLTYPAHGWDSINEV 59

NOV2:  61  DESFQPIHTYQVCNVMSPNQNNWLRTSWVPRDGARRVYAEIKFTLRDCNSMPGVLGTCKE 120
           ||||+|||||||||||||||||||+|||||||||||||||||||||+|||||||||
Sbjct:  60  DESFRPIHTYQVCNVMSPNQNNWLRTNWVPRDGARRVYAEIKFTLRDCNSIPGVLGTCKE 119

NOV2:  121 TFNLYYLESDRDLGASTQESQFLKIDTIAADESFTGADLGVRRLKLNTEVRSVGPLSKRG 180
           ||||+|||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct:  120 TFNLHYLESDRDLGASTQESQFLKIDTIAADESFTGADLGVRRLKLNTEVRGVGPLSKRG 179

NOV2:  181 FYLAFQDIGACLAILSLRIYYKKCPAMVRNLAAFSEAVTGADSSSLVEVRGQCVRHSEER 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  180 FYLAFQDIGACLAILSLRIYYKKCPAMVRNLAAFSEAVTGADSSSLVEVRGQCVRHSEER 239

NOV2:  241 DTPKMYCSAEGEWLVPIGKCVCSAGYEERRDACVACELGFYKSAPGDQLCARCPPHSHSA 300
           |||||||||||||||||||||||||||||+||||||||||||||||||||||||||||
Sbjct:  240 DTPKMYCSAEGEWLVPIGKCVCSAGYEERRDACMACELGFYKSAPGDQLCARCPPHSHSA 299

NOV2:  301 APAAQACHCDLSYYRAALDPPSSACTRPPSAPVNLISSVNGTSVTLEWAPPLDPGGRSDI 360
           ||||  |  |||||||||||||+|||||||||||||||||||||||||||||||||||||
Sbjct:  300 TPAAQTCRCDLSYYRAALDPPSAACTRPPSAPVNLISSVNGTSVTLEWAPPLDPGGRSDI 359

NOV2:  361 TYNAVCRRCPWALSRCEACGSGTRFVPQQTSLVQASLLVANLLAHMNYSFWIEAVNGVSD 420
           |||||||||||||| |||||||||||||||| |||||||||||||||||||||||||+
Sbjct:  360 TYNAVCRRCPWALSHCEACGSGTRFVPQQTSLAQASLLVANLLAHMNYSFWIEAVNGVSN 419

NOV2:  421 LSPEPRRAAVVNITTNQAAPSQVVVIRQERAGQTSVSLLWQEPEQPNGIILEYEIKYYEK 480
           ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  420 LSPEPRSAAVVNITTNQAAPSQVVVIRQERAGQTSVSLLWQEPEQPNGIILEYEIKYYEK 479

NOV2:  481 DKEMQSYSTLKAVTTRATVSGLKPGTRYVFQVRARTSAGCGRFSQAMEVETGKPRPRYDT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  480 DKEMQSYSTLKAVTTRATVSGLKPGTRYVFQVRARTSAGCGRFSQAMEVETGKPRPRYDT 539

NOV2:  541 RTIVWICLTLITGLVVLLLLLICKKRHCGYSKAFQDSDEEKMHYQNGQAPPPVFLPLHHP 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||+||
Sbjct:  540 RTIVWICLTLITGLVVLLLLLICKKRHCGYSKAFQDSDEEKMHYQNGQAPPPVFLPLNHP 599

NOV2:  601 PGKLPEPQFYAEPHTYEEPGRAGRSFTREIEASRIHIEKIIGSGDSGEVCYGRLRVPGQR 660
           |||  ||  ||  |||||||||||||||||||||||||||||||+|||||||||+|||||
Sbjct:  600 PGKFPETQFSAEPHTYEEPGRAGRSFTREIEASRIHIEKIIGSGESGEVCYGRLQVPGQR 659

NOV2:  661 DVPVAIKALKAGYTERQRRDFLSEASIMGQFDHPNIIRLEGVVTRGRLAMIVTEYMENGS 720
           ||||||||||||||||+||||||+|||||||||||||||||||||||||||||||||||
Sbjct:  660 DVPVAIKALKAGYTERQRQDFLSEAAIMGQFDHPNIIRLEGVVTRGRLAMIVTEYMENGS 719

NOV2:  721 LDTFLRTHDGQFTIMQLVGMLRGVGAGMRYLSDLGYVHRDLAARNVLVDSNLVCKVSDFG 780
           ||  ||||||||||+|||||||||||||||||||+||||||||||   |||||||||
Sbjct:  720 LDAFLRTHDGQFTIVQLVGMLRGVGAGMRYLSDLGYIHRDLAARNVLVDGRLVCKVSDFG 779

NOV2:  781 LSRVLEDDPDAAYTTTGGKIPIRWTAPEAIAFRTFSSASDVWSFGVVMWEVLAYGERPYW 840
           |||  |||||+|||||  ||||||||||||||||||||||||||||||||||||||||||
Sbjct:  780 LSRALEDDPEAAYTTAGGKIPIRWTAPEAIAFRTFSSASDVWSFGVVMWEVLAYGERPYW 839

NOV2:  841 NMTNRDVISSVEEGYRLPAPMGCPHALHQLMLDCWHKDRAQRPRFSQIVSVLDALIRSPE 900
           ||||+|||||||||||||||||  ||||||||||||||||||+ +|||||||+ |||
Sbjct:  840 NMTNQDVISSVEEGYRLPAPMGCPRALHQLMLDCWHKDRAQRPRFAHVVSVLDALVHSPE 899

NOV2:  901 SLRATATVSRCPPPAFVRSCFDLRGGSGGGGGLTVGDWLDSIRMGRYRDHFAAGGYSSLG 960
           ||||||||||||||| |||||||  |  | | ||||||||||||||||||||||||||||
```

```
Sbjct: 900 SLRATATVSRCPPPAFARSCFDLRAGGSGNGDLTVGDWLDSIRMGRYRDHFAAGGYSSLG 959

NOV2:  961 MVLRMNAQDVRALGITLMGHQKKILGSIQTMR 992 (SEQ ID NO:5)
           |||||||||||||||||||||||||||||||
Sbjct: 960 MVLRMNAQDVRALGITLMGHQKKILGSIQTMR 991 (SEQ ID NO:52)
```

Beginning on page 14, please replace Table 6A with the following Table 6A:

Table 6A.
Comparison between a NOV2 polypeptide and human ephrin receptor EphA8

```
>ref|NP_065387.1| EphA8; Ephrin receptor EphA8 (eph- and elk-related kinase); Hek3;
          eph-, elk-related tyrosine kinase; ephrin receptor EphA8
 emb|CAB81612.1| (AL035703) dJ61A9.1 (tyrosine kinase ) [Homo sapiens]
          Length = 1005

 Score = 2054 bits (5262), Expect = 0.0
 Identities = 992/992 (100%), Positives = 992/992 (100%)

NOV2 : 1   MAPARGRLPPALWVVTAAAAAATCVSAARGEVNLLDTSTIHGDWGWLTYPAHGWDSINEV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1   MAPARGRLPPALWVVTAAAAAATCVSAARGEVNLLDTSTIHGDWGWLTYPAHGWDSINEV 60

NOV2 : 61  DESFQPIHTYQVCNVMSPNQNNWLRTSWVPRDGARRVYAEIKFTLRDCNSMPGVLGTCKE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61  DESFQPIHTYQVCNVMSPNQNNWLRTSWVPRDGARRVYAEIKFTLRDCNSMPGVLGTCKE 120

NOV2 : 121 TFNLYYLESDRDLGASTQESQFLKIDTIAADESFTGADLGVRRLKLNTEVRSVGPLSKRG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121 TFNLYYLESDRDLGASTQESQFLKIDTIAADESFTGADLGVRRLKLNTEVRSVGPLSKRG 180

NOV2 : 181 FYLAFQDIGACLAILSLRIYYKKCPAMVRNLAAFSEAVTGADSSSLVEVRGQCVRHSEER 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181 FYLAFQDIGACLAILSLRIYYKKCPAMVRNLAAFSEAVTGADSSSLVEVRGQCVRHSEER 240

NOV2 : 241 DTPKMYCSAEGEWLVPIGKCVCSAGYEERRDACVACELGFYKSAPGDQLCARCPPHSHSA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 241 DTPKMYCSAEGEWLVPIGKCVCSAGYEERRDACVACELGFYKSAPGDQLCARCPPHSHSA 300

NOV2 : 301 APAAQACHCDLSYYRAALDPPSSACTRPPSAPVNLISSVNGTSVTLEWAPPLDPGGRSDI 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301 APAAQACHCDLSYYRAALDPPSSACTRPPSAPVNLISSVNGTSVTLEWAPPLDPGGRSDI 360

NOV2 : 361 TYNAVCRRCPWALSRCEACGSGTRFVPQQTSLVQASLLVANLLAHMNYSFWIEAVNGVSD 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 361 TYNAVCRRCPWALSRCEACGSGTRFVPQQTSLVQASLLVANLLAHMNYSFWIEAVNGVSD 420

NOV2 : 421 LSPEPRRAAVVNITTNQAAPSQVVVIRQERAGQTSVSLLWQEPEQPNGIILEYEIKYYEK 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 421 LSPEPRRAAVVNITTNQAAPSQVVVIRQERAGQTSVSLLWQEPEQPNGIILEYEIKYYEK 480

NOV2 : 481 DKEMQSYSTLKAVTTRATVSGLKPGTRYVFQVRARTSAGCGRFSQAMEVETGKPRPRYDT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 481 DKEMQSYSTLKAVTTRATVSGLKPGTRYVFQVRARTSAGCGRFSQAMEVETGKPRPRYDT 540

NOV2 : 541 RTIVWICLTLITGLVVLLLLLICKKRHCGYSKAFQDSDEEKMHYQNGQAPPPVFLPLHHP 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 541 RTIVWICLTLITGLVVLLLLLICKKRHCGYSKAFQDSDEEKMHYQNGQAPPPVFLPLHHP 600

NOV2 : 601 PGKLPEPQFYAEPHTYEEPGRAGRSFTREIEASRIHIEKIIGSGDSGEVCYGRLRVPGQR 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 601 PGKLPEPQFYAEPHTYEEPGRAGRSFTREIEASRIHIEKIIGSGDSGEVCYGRLRVPGQR 660
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NOV2 : 661 DVPVAIKALKAGYTERQRRDFLSEASIMGQFDHPNIIRLEGVVTRGRLAMIVTEYMENGS 720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 661 DVPVAIKALKAGYTERQRRDFLSEASIMGQFDHPNIIRLEGVVTRGRLAMIVTEYMENGS 720

NOV2 : 721 LDTFLRTHDGQFTIMQLVGMLRGVGAGMRYLSDLGYVHRDLAARNVLVDSNLVCKVSDFG 780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 721 LDTFLRTHDGQFTIMQLVGMLRGVGAGMRYLSDLGYVHRDLAARNVLVDSNLVCKVSDFG 780

NOV2 : 781 LSRVLEDDPDAAYTTTGGKIPIRWTAPEAIAFRTFSSASDVWSFGVVMWEVLAYGERPYW 840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 781 LSRVLEDDPDAAYTTTGGKIPIRWTAPEAIAFRTFSSASDVWSFGVVMWEVLAYGERPYW 840

NOV2 : 841 NMTNRDVISSVEEGYRLPAPMGCPHALHQLMLDCWHKDRAQRPRFSQIVSVLDALIRSPE 900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 841 NMTNRDVISSVEEGYRLPAPMGCPHALHQLMLDCWHKDRAQRPRFSQIVSVLDALIRSPE 900

NOV2 : 901 SLRATATVSRCPPPAFVRSCFDLRGGSGGGGGLTVGDWLDSIRMGRYRDHFAAGGYSSLG 960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 901 SLRATATVSRCPPPAFVRSCFDLRGGSGGGGGLTVGDWLDSIRMGRYRDHFAAGGYSSLG 960

NOV2 : 961 MVLRMNAQDVRALGITLMGHQKKILGSIQTMR 992 (SEQ ID NO:5)
           |||||||||||||||||||||||||||||||
Sbjct: 961 MVLRMNAQDVRALGITLMGHQKKILGSIQTMR 992 (SEQ ID NO:53)
```

On page 16, kindly replace the paragraph in Table 7 beginning at line 4 with the following:

Table 7 shows multiple sequence alignment of the NOV2 ephrim type-A receptor 8-like protein of the invention, shown as AL035703 Spliced2 , with similar proteins. The various aligned proteins are as follows: AL035703 Spliced2 (SEQ ID NO:5) with several proteins: EPA8 Mouse (SEQ ID NO:54), EPA5 Human (SEQ ID NO:55) and EPA5 Chick (SEQ ID NO:56). (Black outlined amino acids indicate potential regions of conserved sequence; greyed amino acids represent amino acids conservatively substituted; and non-highlighted amino acids indicate positions in which mutations to a broad range of alternative amino acid residues occurs)

On page 20, please replace the paragraph in Table 9 beginning at line 5 with the following:

Table 9 shows sequence alignment between a NOV3 polypeptide with several members of the human fibronectin leucine repeat transmembrane family: AAF28461.1|AF169 (SEQ ID NO:57), AAF28460.1|AF169 (SEQ ID NO:58) and AAF28459.1|AF169 (SEQ ID NO:59). (Black outlined amino acids indicate potential regions of conserved sequence; greyed amino acids represent amino acids conservatively substituted; and non-highlighted amino acids indicate positions in which mutations to a broad range of alternative amino acid residues occurs)

On page 21, kindly replace Table 9. continued with the following Table 9A:

TABLE 9A.

```
>ref|NP_037412.1| fibronectin leucine rich transmembrane protein 1
 gb|AAF28459.1|AF169675_1 (AF169675) leucine-rich repeat transmembrane protein FLRT1
[Homo
          sapiens]
         Length = 674

 Score = 1365 bits (3494), Expect = 0.0
Identities = 673/674 (99%), Positives = 674/674 (99%)

NOV3:  1   MVVAHPTATATTTPTATVTATVVMTTATMDLRDWLFLCYGLIAFLTEVIDSTTCPSVCRC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1   MVVAHPTATATTTPTATVTATVVMTTATMDLRDWLFLCYGLIAFLTEVIDSTTCPSVCRC 60

NOV3:  61  DNGFIYCNDRGLTSIPADIPDDATTLYLQNNQINNAGIPQDLKTKVNVQVIYLYENDLDE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61  DNGFIYCNDRGLTSIPADIPDDATTLYLQNNQINNAGIPQDLKTKVNVQVIYLYENDLDE 120

NOV3:  121 FPINLPRSLRELHLQDNNVRTIARDSLARIPLLEKLHLDDNSVSTVSIEEDAFADSKQLK 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121 FPINLPRSLRELHLQDNNVRTIARDSLARIPLLEKLHLDDNSVSTVSIEEDAFADSKQLK 180

NOV3:  181 LLFLSRNHLSSIPSGLPHTLEELRLDDNRISTIPLHAFKGLNSLRRLVLDGNLLANQRIA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181 LLFLSRNHLSSIPSGLPHTLEELRLDDNRISTIPLHAFKGLNSLRRLVLDGNLLANQRIA 240

NOV3:  241 DDTFSRLQNLTELSLVRNSLAAPPLNLPSAHLQKLYLQDNAISHIPYNTLAKMRELERLD 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 241 DDTFSRLQNLTELSLVRNSLAAPPLNLPSAHLQKLYLQDNAISHIPYNTLAKMRELERLD 300

NOV3:  301 LSNNNLTTLPRGLFDDLGNLAQLLLRNNPWFCGCNLMWLRDWVKARAAVVNVRGLMCQGP 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301 LSNNNLTTLPRGLFDDLGNLAQLLLRNNPWFCGCNLMWLRDWVKARAAVVNVRGLMCQGP 360

NOV3:  361 EKVRGMAIKDITSEMDECFETGPQGGVANAAAKTTASNHASATTPQGSLFTLKAKRPGLR 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 361 EKVRGMAIKDITSEMDECFETGPQGGVANAAAKTTASNHASATTPQGSLFTLKAKRPGLR 420

NOV3:  421 LPDSNIDYPMATGDGAKTLAIHVKALTADSIRITWKATLPASSFRLSWLRLGHSPAVGSI 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 421 LPDSNIDYPMATGDGAKTLAIHVKALTADSIRITWKATLPASSFRLSWLRLGHSPAVGSI 480

NOV3:  481 TETLVQGDKTEYLLTALEPKSTYIICMVTMETSNAYVADETPVCAKAETADSYGPTTTLN 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 481 TETLVQGDKTEYLLTALEPKSTYIICMVTMETSNAYVADETPVCAKAETADSYGPTTTLN 540

NOV3:  541 QEQNAGPMASLPLAGIIGGAVALVFLFLVLGAICWYVHQAGELLTRERAYNRGSRKKDDY 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||+||||
Sbjct: 541 QEQNAGPMASLPLAGIIGGAVALVFLFLVLGAICWYVHQAGELLTRERAYNRGSREKDDY 600

NOV3:  601 MESGTKKDNSILEIRGPGLQMLPINPYRAKEEYVVHTIFPSNGSSLCKATHTIGYGTTRG 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 601 MESGTKKDNSILEIRGPGLQMLPINPYRAKEEYVVHTIFPSNGSSLCKATHTIGYGTTRG 660

NOV3:  661 YRDGGIPDIDYSYT 674 (SEQ ID NO:7)
           ||||||||||||||
Sbjct: 661 YRDGGIPDIDYSYT 674 (SEQ ID NO:60)
```

On page 22, please replace the paragraph in Table 10 beginning at line 6 with the following: